

SEQUENCE LISTING

<110> Lorantis Limited
Briend, Emmanuel CP
Champion, Brian R
Solari, Roberto CE

<120> Modulators

<130> 674525-2011

<140> PCT/GB02/04390

<141> 2002-09-27

<150> GB 0123379.0

<151> 2001-09-28

<160> 9

<170> PatentIn version 3.1

<210> 1

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Oligonucleotide

<400> 1

tcgtcgtttt gtcgttttgt cggt

24

<210> 2

<211> 864

<212> PRT

<213> Artificial sequence

<220>

<223> hDelta1-IgG4Fc fusion protein

<400> 2

Met Gly Ser Arg Cys Ala Leu Ala Leu Ala Val Leu Ser Ala Leu Leu
1 5 10 15

Cys Gln Val Trp Ser Ser Gly Val Phe Glu Leu Lys Leu Gln Glu Phe
20 25 30

Val Asn Lys Lys Gly Leu Leu Gly Asn Arg Asn Cys Cys Arg Gly Gly
35 40 45

Ala Gly Pro Pro Pro Cys Ala Cys Arg Thr Phe Phe Arg Val Cys Leu
50 55 60

Lys His Tyr Gln Ala Ser Val Ser Pro Glu Pro Pro Cys Thr Tyr Gly
65 70 75 80

Ser Ala Val Thr Pro Val Leu Gly Val Asp Ser Phe Ser Leu Pro Asp
85 90 95

Gly Gly Gly Ala Asp Ser Ala Phe Ser Asn Pro Ile Arg Phe Pro Phe
100 105 110

Gly Phe Thr Trp Pro Gly Thr Phe Ser Leu Ile Ile Glu Ala Leu His
115 120 125

Thr Asp Ser Pro Asp Asp Leu Ala Thr Glu Asn Pro Glu Arg Leu Ile
130 135 140

Ser Arg Leu Ala Thr Gln Arg His Leu Thr Val Gly Glu Glu Trp Ser
145 150 155 160

Gln Asp Leu His Ser Ser Gly Arg Thr Asp Leu Lys Tyr Ser Tyr Arg
165 170 175

Phe Val Cys Asp Glu His Tyr Tyr Gly Glu Gly Cys Ser Val Phe Cys
180 185 190

Arg Pro Arg Asp Asp Ala Phe Gly His Phe Thr Cys Gly Glu Arg Gly
195 200 205

Glu Lys Val Cys Asn Pro Gly Trp Lys Gly Pro Tyr Cys Thr Glu Pro
210 215 220

Ile Cys Leu Pro Gly Cys Asp Glu Gln His Gly Phe Cys Asp Lys Pro
225 230 235 240

Gly Glu Cys Lys Cys Arg Val Gly Trp Gln Gly Arg Tyr Cys Asp Glu
245 250 255

Cys Ile Arg Tyr Pro Gly Cys Leu His Gly Thr Cys Gln Gln Pro Trp
260 265 270

Gln Cys Asn Cys Gln Glu Gly Trp Gly Gly Leu Phe Cys Asn Gln Asp
275 280 285

Leu Asn Tyr Cys Thr His His Lys Pro Cys Lys Asn Gly Ala Thr Cys
290 295 300

Thr Asn Thr Gly Gln Gly Ser Tyr Thr Cys Ser Cys Arg Pro Gly Tyr
305 310 315 320

Thr Gly Ala Thr Cys Glu Leu Gly Ile Asp Glu Cys Asp Pro Ser Pro
325 330 335

Cys Lys Asn Gly Gly Ser Cys Thr Asp Leu Glu Asn Ser Tyr Ser Cys
340 345 350

Thr Cys Pro Pro Gly Phe Tyr Gly Lys Ile Cys Glu Leu Ser Ala Met
355 360 365

Thr Cys Ala Asp Gly Pro Cys Phe Asn Gly Gly Arg Cys Ser Asp Ser
370 375 380

Pro Asp Gly Gly Tyr Ser Cys Arg Cys Pro Val Gly Tyr Ser Gly Phe
385 390 395 400

Asn Cys Glu Lys Lys Ile Asp Tyr Cys Ser Ser Ser Pro Cys Ser Asn
405 410 415

Gly Ala Lys Cys Val Asp Leu Gly Asp Ala Tyr Leu Cys Arg Cys Gln
420 425 430

Ala Gly Phe Ser Gly Arg His Cys Asp Asp Asn Val Asp Asp Cys Ala
435 440 445

Ser Ser Pro Cys Ala Asn Gly Gly Thr Cys Arg Asp Gly Val Asn Asp
450 455 460

Phe Ser Cys Thr Cys Pro Pro Gly Tyr Thr Gly Arg Asn Cys Ser Ala
465 470 475 480

Pro Val Ser Arg Cys Glu His Ala Pro Cys His Asn Gly Ala Thr Cys
485 490 495

His Glu Arg Gly His Gly Tyr Val Cys Glu Cys Ala Arg Gly Tyr Gly
500 505 510

Gly Pro Asn Cys Gln Phe Leu Leu Pro Glu Leu Pro Pro Gly Pro Ala
515 520 525

Val Val Asp Leu Thr Glu Lys Leu Glu Ala Ser Thr Lys Gly Pro Ser
530 535 540

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
545 550 555 560

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
565 570 575

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
580 585 590

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
595 600 605

Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His
610 615 620

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly
625 630 635 640

Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser
645 650 655

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
660 665 670

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro
675 680 685

Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
690 695 700

Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val
705 710 715 720

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
725 730 735

Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr

740

745

750

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 755 760 765

Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
 770 775 780

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 785 790 795 800

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 805 810 815

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser
 820 825 830

Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 835 840 845

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 850 855 860

<210> 3
 <211> 26
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Adenovirus major late promoter TATA-box motif with BglIII and Hind
 III cohesive ends

<400> 3
 gatctggggg gctataaaag ggggta 26

<210> 4
 <211> 26
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Adenovirus major late promoter TATA-box motif with BglIII and Hind
 III cohesive ends

<400> 4
 agcttacccc cttttatagc ccccca 26

<210> 5
 <211> 50
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> TP1 promoter sequence with BamH1 and BglII cohesive ends

 <400> 5
 gatccccgact cgtgggaaaaa tgggcggaag ggcaccgtgg gaaaatagta 50

 <210> 6
 <211> 50
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> TP1 promoter sequence with BamH1 and BglII cohesive ends

 <400> 6
 gatctactat tttcccacgg tgcccttccg cccattttcc caccagtcgg 50

 <210> 7
 <211> 43
 <212> PRT
 <213> Artificial sequence

 <220>
 <223> DSL domain

 <220>
 <221> MISC_FEATURE
 <222> 2..4, 7..9, 11..13, 20, 24, 25, 27..29, 31..33
 <223> Xaa may be any amino acid

 <220>
 <221> MISC_FEATURE
 <222> 35, 36, 38, 39, 41, 42
 <223> Xaa may be any amino acid

 <220>
 <221> MISC_FEATURE
 <222> 5, 6, 21, 23
 <223> Xaa may be any amino acid, preferably an aromatic amino acid residue,
 such as Tyr, Phe, Trp or His

 <220>
 <221> MISC_FEATURE
 <222> 16, 22, 30, 37, 40
 <223> Xaa may be any amino acid, preferably a non polar amino acid
 residue, such as Gly, Ala, Pro, Leu, Ile or Val

<220>
 <221> MISC_FEATURE
 <222> (15, 17)
 <223> Xaa may be any amino acid, preferably a basic amino acid residue
 such as Arg or Lys

<220>
 <221> MISC_FEATURE
 <222> (18, 19)
 <223> Xaa may be any amino acid, preferably an acid or amide amino acid
 residue such as Asp, Glu, Asn or Gln

<400> 7

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30

Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
 35 40

<210> 8
 <211> 43
 <212> PRT
 <213> Artificial sequence

<220>
 <223> DSL domain

<220>
 <221> MISC_FEATURE
 <222> 2..4, 7..9, 11..13, 20, 24, 25, 27..29, 31..33
 <223> Xaa may be any amino acid

<220>
 <221> MISC_FEATURE
 <222> 35, 36, 39, 41, 42
 <223> Xaa may be any amino acid

<400> 8

Cys Xaa Xaa Xaa Tyr Tyr Xaa Xaa Xaa Cys Xaa Xaa Xaa Cys Arg Pro
 1 5 10 15

Arg Asx Asp Xaa Phe Gly His Xaa Xaa Cys Xaa Xaa Xaa Gly Xaa Xaa
 20 25 30

Xaa Cys Xaa Xaa Gly Trp Xaa Gly Xaa Xaa Cys
35 40

<210> 9
<211> 175
<212> PRT
<213> Artificial sequence

<220>
<223> Typical EGF-like domain

<220>
<221> DISULFID
<222> (5)..(67)
<223>

<220>
<221> DISULFID
<222> (54)..(138)
<223>

<220>
<221> DISULFID
<222> (145)..(174)
<223>

<220>
<221> MISC_FEATURE
<222> 1..4, 6..53, 55..66, 68..137, 139..144, 146, 147
<223> Xaa is any residue

<220>
<221> MISC_FEATURE
<222> 150..170, 172, 173
<223> Xaa is any residue

<220>
<221> MISC_FEATURE
<222> (149)..(149)
<223> Xaa is an often conserved aromatic amino acid

<220>
<221> MISC_FEATURE
<222> 6..53, 150..170
<223> Xaa may be present or absent

<220>
<221> MISC_FEATURE
<222> 55..66

<223> Any 9 Xaas may be absent - indicates a range of 3 - 12 amino acids

<220>

<221> MISC_FEATURE

<222> 68..137

<223> Any 69 Xaas may be absent - indicates a range of 1 - 70 amino acids

<220>

<221> MISC_FEATURE

<222> 139..144

<223> Any 5 Xaas may be absent - indicates a range of 1 - 6 amino acids

<400> 9

Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5					10					15	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20					25					30		

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		35					40					45			

Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
	50					55					60				

Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
65					70				75						80

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				85					90					95	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				100					105					110	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				115					120				125		

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		130					135				140				

Cys	Xaa	Xaa	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
145					150					155					160

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Xaa	Cys	Xaa	
				165						170				175	